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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                        272.5
262.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb
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Match
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                                                                                374700 seqs, 117207915 residues
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fungi:*
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sp_vertebrate:*
sp_virus:*
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Q54953 streptococc
Q33709 streptococc
Q01924 streptococc
Q47942 streptococc
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P79883	Q9w3d6	085085	Q2318 [°]	Q9u347	03070	Q9z1g	.0pqe0	Q9ki13	06120	03064	Q9rp10	Q45616	07002	666980	Q9vaf5	Q9ppt2	086488	Q9×3m7	Q4603	Q9rn43	Q9ppz!	Q9rgn5	Q48588	P72534	085088
83 xenopus. ma	6 drosophila	5 moraxella c	7 caenorhabdi		4 mycoplasma	7	9	3 staphylococ		3 mycoplasma		6 bacillus su						7 streptococc	*	ω	5 ureaplasma	5 lactobacill	8 lactococcus	4 streptococc	8 moraxella c

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                                                                                                               Query Match
Best Local Sim
Matches 203;
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                                                                                                                                                                                                                                                     MEDLINE-95020565; PubMed-7934855;

Sela S., Aviv A., Burstien I., Tovi A., Caparon M.G., Hanski E.;

"Protein F: an adhesin of Streptococcus pyogenes binds fibronectin via two distinct domains.";

Mol. Microbiol. 10:1049-1055(1993).

EMBL; L10919; AAAA26964.1; -

INTERPRO; IPR001899; -

PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

SEQUENCE 659 AA; 73628 MW; DOCEB91D159726BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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24 TKRKRRFAVTLYGVFFMLLACAGAIGFGQVAYAADEKTVPSHSSP--NPEFPWYGYDAYG 81
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                                                                                                                                              Local Similarity
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                                                    SKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAINPDSSSEYRWYGYESYV 79
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                                                                                                                  Conservative 128;
                                                                                                         16.1%; Score 633.5; DB 2; Length 659; 26.1%; Pred. No. 1.4e-29; tive 128; Mismatches 237; Indels 211; Gaps
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Last annotation update)
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                                                                             4
                                                                                                                   KNITPILPATGDIENVLAFLGILILSVLSI 673
                                                                                                                                                                                            GLPEGYSYLVKETDSEGYKVKVNSQEVANATVSKTGITSDETLAFENNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EPVVP-TGVDQKINGYLALIVIAGISL
                                                                                                                                                                                                                                              RKTVTGLAGDRTKDFHFEIELKNNKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQ
                                                                                                                                                                                                                                                                                                 LVEYAQDSNPPQLTDLDFFIPNNNKYQSLIGTQWHPEDLVDIIRMEDKKEVIPVTHNLTL
                                                                                                                                                                                                                                                                                                                         GVLMGGQ-----SESVEFTKDTQAGMSGQTTPQVETEETKEPGVLMGGQSES-----
                                                                                                                                                                                                                                                                                                                                                  QLRAATQLAIYYFTDSAELDKDKLKDYHG------FGDMNDSTLAVAKI
                                                                                                                                                                                                                                                                                                                                                                            ----SGETDYI----IEVYGNQQNPVDIDK-----KLPNETGF--SGNMVETEETKEP
                                                                                                                                                                                                                                                                                                                                                                                                    PDFTTGEVKYTHIAGRDLFKYTVKPRDTDPDTFLKHIKKVIEKGYREKGQAIEYSGLTET
                                                                                                                                                                                                                                                                                                                                                                                                                               DLPIEVPRYE --
                                                                                                                                                                                                                                                                                                                                                                                                                                                        E-PYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVVYCFNADLKSPPDSEDGGKTMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -QEVPEVPSESLEPALPPLMPELDGEEIPEVPSESLEPALPPLMPELDGQEV--PEKPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYTLTELNSPAGYSIAEPITFKVEAGKVYTI-------IDGKQIENPNKEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDGEEVPEVPSESLEPALPPLVPELDGEEVPEVPS----ESLEPALPPLMPELDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTSVLIRKYAIGDYSKLLEGATLQLTGDNVNSFQARVFSSNDIGERIELS------DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KSYQNLLSAEYVPDDPPKPGDTSEHNPKTPELDGTPIPEDPKRPDESSGPALPPLMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNKGYQNLLSGGLVPTKPPTPGD-------PPMPPNQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNFFTSEANDLNIPPQQLTLMREALRKLISSDENLV----KQVPSNFKLSIFESSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAENPRFSGEELRRHILKVLYNGYP-NSNEIMKGIDPLNAILVTQNAIWYYSDSAPINDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRLLRY - - - - - - HNLKVN - - GSKEYQAYCFNLKRFEPKKEESSSPNWYKKLDGSTETFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKRKRRFAVTLVGVFFMLFACAGSIGFGQVAYAADEKTEPNRIN--SNPEFPWYGYDSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAINPDSSSEYRWYGYESYV
                                                                                                                                                                                                                                                                       -VEFTKDT----PEV----QTGMSGQTAPQ----VETEDTKE--PEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IPR001899; -.
PS00343; GRAM_POS_ANCHORING; UNKNOWN_1
685 AA; 75988 MW; 9F4633A35C5D4DD3
(TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                       LMGGQSESVEFK - - - KDTQAGMSGQTA - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 117;
                                                    PRELIMINARY;
                                                                                                                                                                    -TQTGSSGFSETVSIVEDTRPKL---
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  13,
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Pred.
Last sequence update)
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No. 3
                                                                                                                                           743
                                                    638
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3.1e-28;
1es 237;
                                                  B
                                                                                                                                                                    ----VFHFDNNEPKVEEHREKPT
                                                                                                                                                                                                                      - PQVETEDTKEPEVLMGGQSESVE
                                                                                                                                                                                                                                                                                                                                                                                                                               FNNKDQSPLAGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Talay S.R., Valentin-Weigand P., Timmis K.N., Chhatwal.G. "Domain structure and conserved epitopes of 5fb protein, fibronectin-binding adhesin of Streptococcus pyogenes."; Mol. Microbiol. 13:531-539(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Fibronectin-binding protein of Streptococcus pyogenes: sequence of the binding domain involved in adherence of streptococci to epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chhatwal G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Talay S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92363585; PubMed=1386839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 371-638 FROM N.A. STRAIN=DSM 2071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95089690; PubMed=7527894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN-BINDING PROTEIN PRECURSOR (SFB PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO;
  129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS IS THE MAJOR GROUP A STREPTOCOCCAL ADHESIN. TH ABILITY OF BACTERIA TO BIND FIBRONECTIN HAS BEEN PROPOSED AS VIRULENCE FACTOR ENABLING BACTERIA TO COLONIZE WOUND TISSUES BLOOD CLOTS. BINDING OF PLASMA FIBRONECTIN TO THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S. PYOGENES THUS REPRESENTING AN IMPORTANT DEFENSE MECHANISM AGAINST TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER STREPTOCOCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CONSTITUENT OF THE CELL WALL. PRESENT ON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVASION. SFB PROTEIN IS INVOLVED TO EPITHELIAL CELLS.
                          YAMSP----RITGDELNOKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A44792; A4479
YADNPRKDNESSRVIDVELEKNILRVLYNGYPNNGNGIMEGLEPLNAILVTQNAVWYYSD
                                                                                       KG-PYTRY----HNLQLNLNGSKTYQAYCFNLKRFEPKKEGSYFPNWYKRWDGSEETFVK 128
                                                                                                                                    RGHPYYKQFRVAHDLRVNLEGSRSYQVYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFED 139
                                                                                                                                                                                 TKRKRRFAVTLVGVFFMLLASAGAIGFGQVAYAADEKTVPHRVS--QNPEFPWYGYDFY-
                                                                                                                                                                                                                       SKNSKRFTVTLVGVFLMIFALVTSMVGAKTVFGLVESSTPNAINPDSSSEYRWYGYESYV 79
                                                                                                                                                                                                                                                                           207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X67947; CAA48133.1;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001899;
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50
421
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633
421
459
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638
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565
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                                                                                                                                                                                                                                                                                                                                                                                       71059 MW;
                                                                                                                                                                                                                                                                                              15.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .'
                                                                                                                                                                                                                                                                        118;
                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                               R4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL WALL-SPANNING REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 X APPROXIMATE TANDEM REPEATS, FIBRONECTIN-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN-BINDING PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEMBRANE ANCHOR REGION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                     D55E2A4E5708F3E0 CRC64;
                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                           No. 8.
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                                                                                                                                                                                                                                                                                           DB 2;
3.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAPHYLOCOCCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADHERENCE
                                                                                                                                                                                                                                                                                                                 Length 638;
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                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                        182;
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Query Match
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Q47942;
Q1-N0V-1996 (TrEMBLrel. 01, C
Q1-NOV-1996 (TrEMBLrel. 01, L
Q1-MAY-2000 (TrEMBLrel. 13, L
FIBRONECTIN BINDING PROTEIN F
                                                                                                                                            group G streptococci.";
Infect. Immun. 64:2122-2129(1996).
EMBL; U31115; AAB06623.1; -.
INTERPRO; IPR001899; -.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 580 AA; 64975 MW; 69994BF415C73A70 CRC64;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-1750;

MEDLINE-96239026; PubMed-8675316;

Kline J.B., Xu S., Bisno A.L., Collins C.M.;

Kline J.B., Xu S., Bisno A.L., Collins C.M.;

"Identification of a fibronectin-binding protein (GfbA) in pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFB.
Streptococcus sp.
Bactleria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 KEPGVLMGGQSESVEFT-----KDTQTGMSGQTTP----QVETEDTKEPGVLMGGQSE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 GFGDMNDSTLAVAKILVEYAQDSNPP-----QLTDLDFFIPNNNKYQSLIGTQWHPEDL 51
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      Conservative
                               13.3%;
      106;
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Last annotation update)
F.
Score 523; DB 2; Length 580;
Pred. No. 3.9e-23;
D6; Mismatches 250; Indels 1
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48		Db Qy	20 SKNSKKETYTLYGYELMLEALYTSMVARKTEVLYESSELMATIGLESTY 79 21 : :: :: :
90		B	81 GAFLRYHDLNVNLEGSTPYQYYCFNLYRQEPSKYNGFRKFRFKKYDGDNAVFKQ
72		Qy Db	140 YAMSPRITGDELNQKLRAVMYNGHPQNANGIMEGLEPLNAIRVTQEAVWYYSDNAPISNP 199 : : : : : : : : : :
14		Qy P	DESFKRESESNLYSTSQLSLMRQALKQLIDPNLATKMPKQVPDDFQLSIFESEDKGDKYN
73		ργ	TGDN
73		Вb	248 NSIQNILSTEYVQDNIQKPGEEP 270
33		Qy	NSFQARVESSNDIGERIELSDGTYTLTELNSPAGYSIAEPITFKVEAGKVYTIIDGKQIE : : : : : : : : :
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87		Qy	NPNKEIVEPYSVEAYNDFEEFSVLTTQNYAKFYYAKNKNGSSQVVYCFNADLKSPP
01		문	
46		ДУ	436 DSEDGGKTMTFDFTTGBYKY THAGKDDEKXYTWREDTDFTEIGHTKNY LENGTKENG 454
05		Qy	QAIEYSGLTETQLRAATQLAIYYFTDSAELDKDKLKDYHGFGDMNDSTLAVAKILVEYAQ : :: ::
98		V 5	555 DSNPPOCITDLDFFIPNNNKYOSLIGTOWHPEDLVDIIRMEDKKEVIPVTHNLTLRKTVTG 614
		Вb	
		Qy	615 LAGDRTKDFHFEIELKNUKQELLSQTVKTDKTNLEFKDGKATINLKHGESLTLQGLPEGY 674
		Db	TEDTKEPGVLMGGQSESVGFT-KDTQTGM
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		γQ	739
		ДЪ	559 GILILS 564
		RESULT 033715	5 G
	•	A U	033715 PRELIMINARY;
			01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
ic			(Tremblrel. 08, BINDING PROTEIN
		88	Streptococcus pyogenes. Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
			D=1314;
			[1] SEQUENCE FROM N.A. STRAIN-M4 STRAIN UMEA:
		RX RA	., Totolian
w	23;	R R	"Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: isolation of the protein and mapping of
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Matches 51; Conserv
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O33711;
O1-73N-1998 (TrEMBLrel. 05, C
O1-JAN-1998 (TrEMBLrel. 05, L
O1 NOV-1998 (TrEMBLrel. 08, L
FIBRONECTIN BINDING PROTEIN F
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01-JAN-1998
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STRAIN-M4 STRAIN 281C;
MEDLINE-98129085; PubMed-9467904;
Katerov V., Andreev A., Schalen C.,
"Protein F, a fibronectin-binding pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pyogenes.
Bacteria; Firmicutes; B
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Microbiology 144:119-126(1998).
EMBL; AF009913; AAC38160.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrembLrel. 05, 01-JAN-1998 (TrembLrel. 05, 01-NOV-1998 (TrembLrel. 08, FIBRONECTIN BINDING PROTEIN
NCBI_TaxID=1314; [1]
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                                                                                          Streptococcus
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STRAIN-M18 STRAIN SS-36;
MEDLINE-98129085; PubMed-9467904;
Katerov V., Andreev A., Schalen C., Totolian A.A.;
"Protein F, a fibronectin-binding protein of Streptococcus also binds human fibrinogen: isolation of the protein and m
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O33721;
O1-JAN-1998 (TREMBLrel. 05, Created)
O1-JAN-1998 (TREMBLrel. 05, Last sequence update)
O1-NOV-1998 (TREMBLrel. 08, Last annotation update)
FIBRONECTIN BINDING PROTEIN F (FRAGMENT).
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STRAIN-M4 STRAIN M4/118;
MEDLINE-98129085; PubMed-9467904;
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Microbiology 144:119-126(1998).
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                                                                                                                                                                                                                                                                                             VYCFNLVRQEPSKVNGFRKNWFKKVDGDNAVFKKYAANPRVIDRRFRTNILNVIYNGY
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116 AA;
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13538 MW;
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12845 MW;
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Pred. No. 2.
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2.1e-06;
3s 42;
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 06,
01-NOV-1998 (TrEMBLrel. 08,
FIBRONECTIN BINDING PROTEIN
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MEDLINE-98129085; PubMed-9467904;
Katerov V., Andreev A., Schalen C.,
"Protein F., a fibronectin-binding po
                                                                                                                                                                            NON_TER
                                                                                                                                                                                                  Microbiology 144:119-126(1998).
EMBL; AF009911; AAC38158.1; -.
                                                                                                                                                                                                                                      Katerov V., Andreev A., Schalen C., Totolian A.A.; "Protein F, a fibronectin-binding protein of Streptococcus also binds human fibrinogen: isolation of the protein and many binds human fibrinogen:
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-M12 STRAIN 100085;
MEDLINE-98129085; PubMed-9467904;
                                                                                                                                                                                                                                                                                                                            Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the binding region.";
Microbiology 144:119-126(1998).
EMBL; AF009917; AAC38164.1; -.
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"Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: isolation of the protein and mapping of
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                                                                                                  Local Similarity
mes 46; Conserv
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                    VYCFNLKKAFPLGSDSSVKKWYKKHDGISTKFEDYAMSPRITGDELNQ
                                                              FGLV----ESSTPNAINPDSSSEYRWYGYESYVRGHPYYKQFRVAHDLRVNLEGSRSYQ 105
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 AYCFNLTKYFPRPTYSTTNNFYKKIDGSGSAFKSYTANPRVLDENLDK 100
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92 AA;
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103 AA;
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10772 MW;
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42.68;
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45.5%;
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F (FRAGMENT).
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Pred. No. 7.8e
17; Mismatches
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Pred. No. 6.
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Query Match Best Local s Matches 46

l Similarity 46; Conserv

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                                                                          Katerov V., Andreev A., Schalen C., Totolian A.A.;
"Protein F, a fibronectin-binding protein of Streptococcus pyogenes
also binds human fibrinogen: isolation of the protein and mapping of
                                                                                      SEQUENCE FROM N.A.
STRAIN-M12 STRAIN 73195/2110;
STRAIN-M2 STRAIN 73195/2110;
MEDLINE-98129085; PubMed-9467904;
Katerov V., Andreev A., Schalen C.,
Katerov V., a fibronectin-binding protein F, a fibronectin-binding protein
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                      the binding region.";
Microbiology 144:119-126(1998).
EMBL; AF009915; AAC38162.1; -.
NON_TER 1
                                                                                                                                                                                                              Streptococcus pyogenes
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Microbiology 144:119-126(1998).
EMBL; AF009918; AAC38165.1; -.
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MEDLINE-98129085; PubMed-9467904;
Katerov V., Andreev A., Schalen C
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NCBI_TaxID=1314;
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102 AA;
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 102 AA;
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ilarity 42.7%;
Conservative 16
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11795 MW;
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F (FRAGMENT).
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Pred. No. 8.8e-06;
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  F6F935A2089DFCFD
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    CRC64;
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Best Local Similarity 44.6%;
Matches 45; Conservative 1
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033713;
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O1-JAN-1998 (TrEMBLrel. 05, Last seq
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FIBRONECTIN BINDING PROTEIN F (FRAGM
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MEDLINE-9819085; PubMed-9467904;
MEDLINE-9819085; PubMed-9467904;
Materov V., Andreev A., Schalen C., Totolian A.A.;
"Protein F, a fibronectin-binding protein of Streptococcus pyogenes,
also binds human fibrinogen: isolation of the protein and mapping of
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Microbiology 144:119-126(1998).
EMBL; AF009919; AAC38166.1; -.
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NCBI_TaxID=1314;
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MEDLINE=98129085; PubMed=9467904;
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11914 MW;
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F (FRAGMENT).
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Pred. No. 1.5e-05;
6; Mismatches 27;
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AECDF38D82AE3EC7 CRC64;
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Best Local Similarity
                  106 VYCENLKKAFPLGSDSSVKKWYKKHDGISTKFEDYAMSPRITGDELNQKL 155
                                     53 VYCFNLVRQEPSKVNGLRKNWFKKVDGHNAVFKKYVANPRVIDGDLERNI 102
                                                                             46;
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                                                                                     Score 204.5; DB Pred. No. 2e-05;
                                                                             Mismatches
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